

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
POLYPEPTIDE...

Okamoto, et al.

Appl. No.: Unknown

Atty Docket: TOYA136.001C1

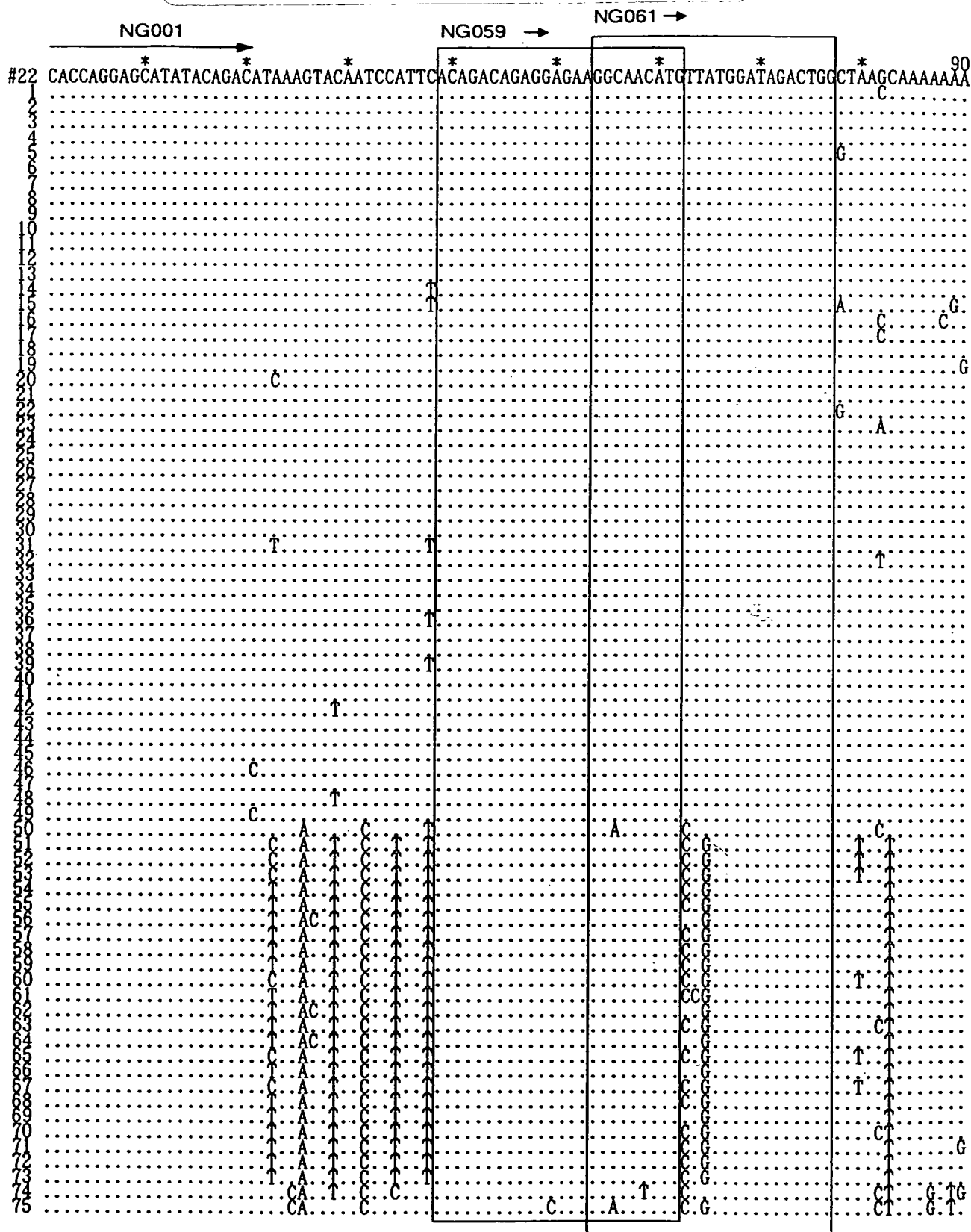


FIG 1

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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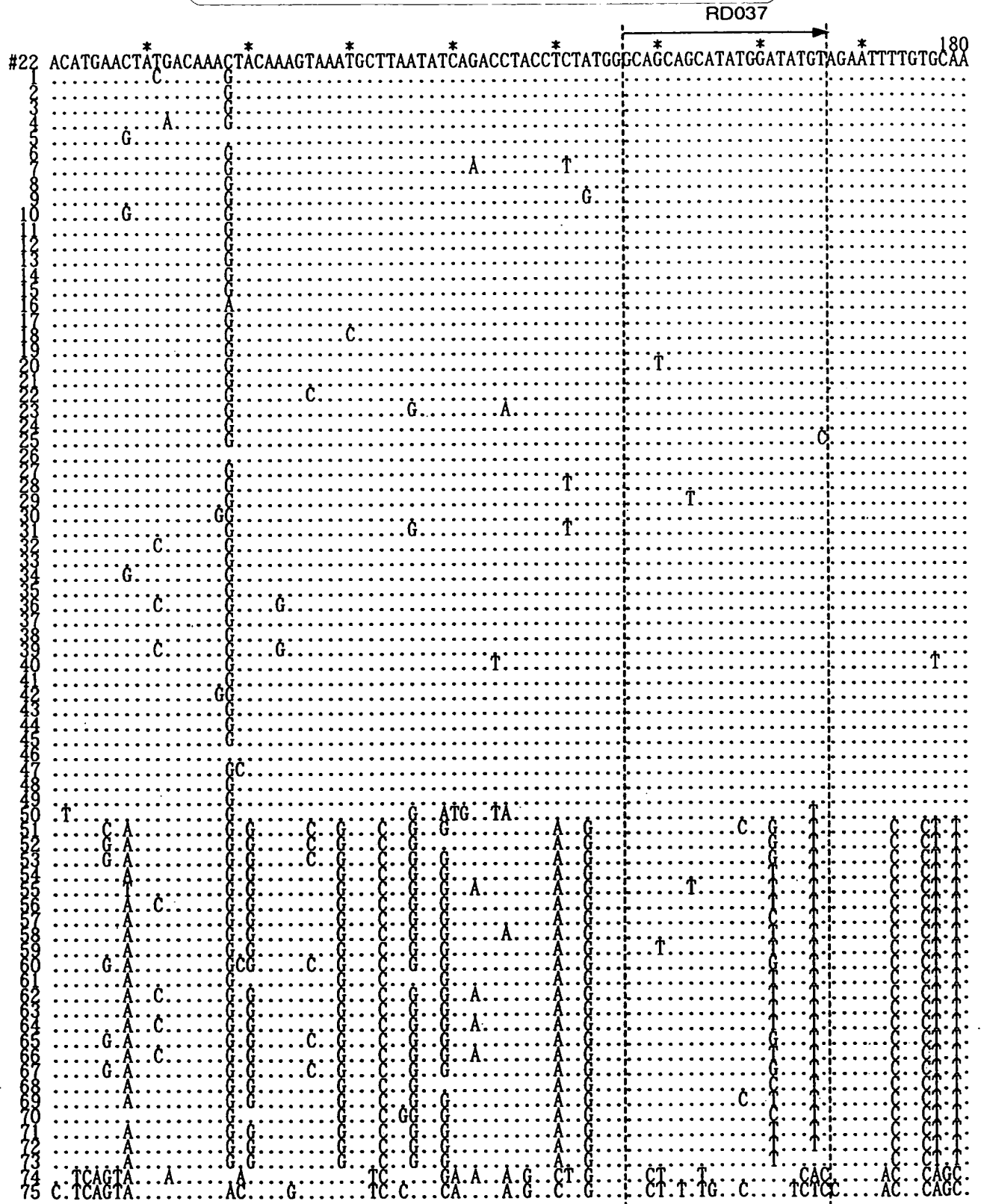


FIG 2

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[illegible]

FIG 3

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[illegible]

FIG 4

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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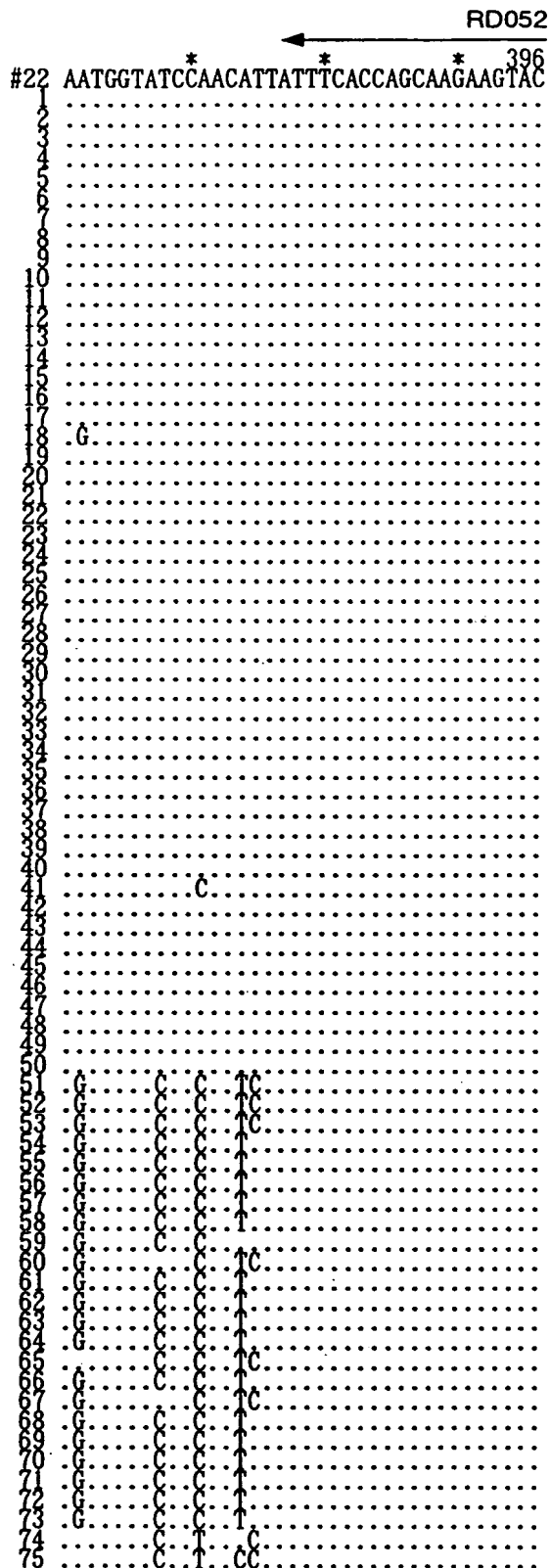


FIG 5

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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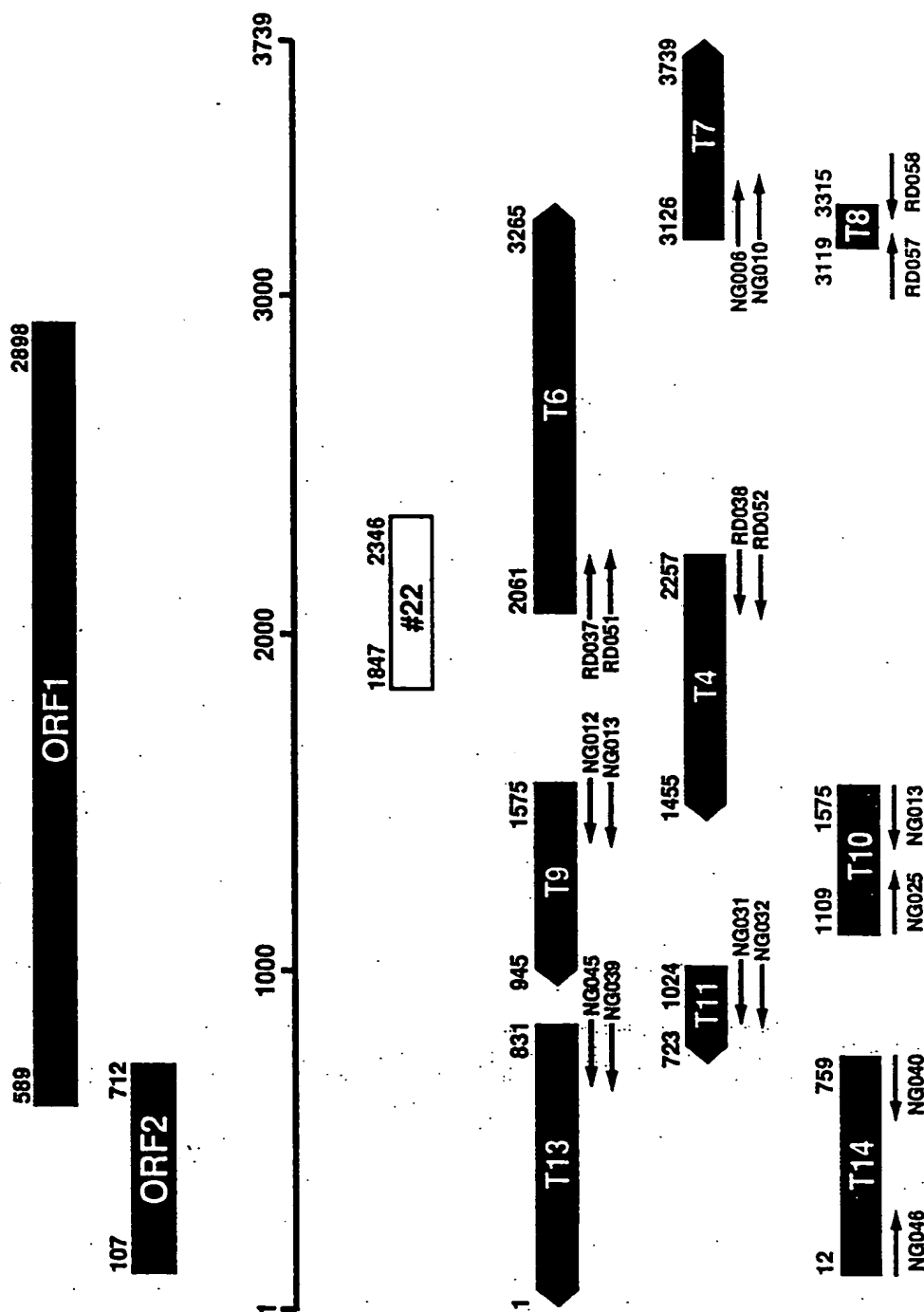


FIG 6

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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```
1) CACCAGGAGCATATACAGACATAAAGTACAATCCATTCCACAGACAGAGGAGGCAACA 60
2) .....
3) .....

1) TGTTATGGATAGACTGGCTAAGCAAAAAAACAATGAACTATGACAAAGTACAAAGTAAAT 120
2) .....
3) .....

1) GCTTAATATCAGACCTACCTCTATGGGCAGCAGCATATGGATATGTAGAATTTGTGCAA 180
2) .....
3) .....

1) AAAGTACAGGAGACCAGAACATACACATGAATGCCAGGCTACTAATAAGAAGTCCCTTTA 240
2) .....
3) .....

1) CAGACCCACAACACTACTAGTACACAGACCCCAAAAGGCTTTGTCCTTACTCTTTAA 300
2) .....
3) .....

1) ACTTTGGAAATGGTAAATGCCAGGAGGTAGTAGTAATGTGCCTATTAGAATGAGAGCTA 360
2) .....
3) .....

1) AATGGTATCCAACATTATTTCCACGAGCAAGAAGTAC 396
2) .....
3) .....
```

- 1) PILOT BLOOD FOR TRANSFUSION
- 2) PATIENT: 2 WEEKS AFTER BLOOD TRANSFUSION
- 3) PATIENT: 4 WEEKS AFTER BLOOD TRANSFUSION

FIG 7

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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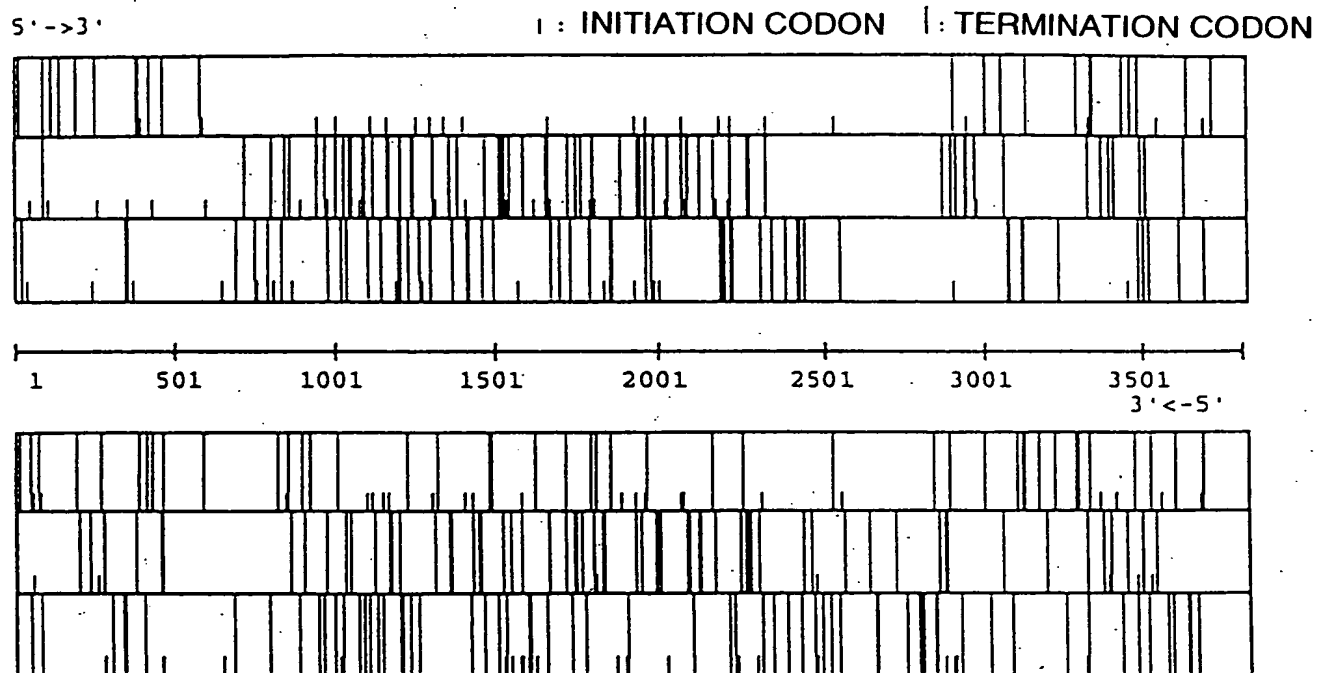


FIG 8

*NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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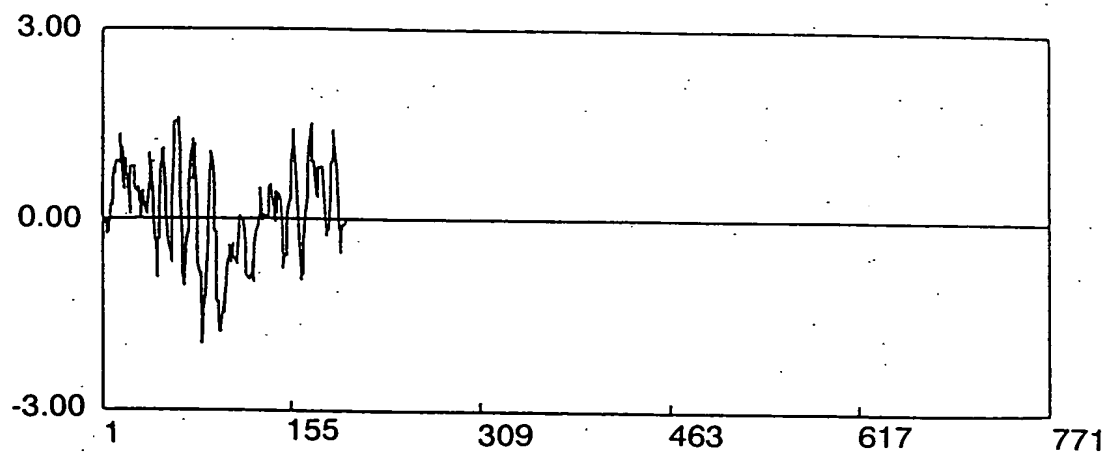
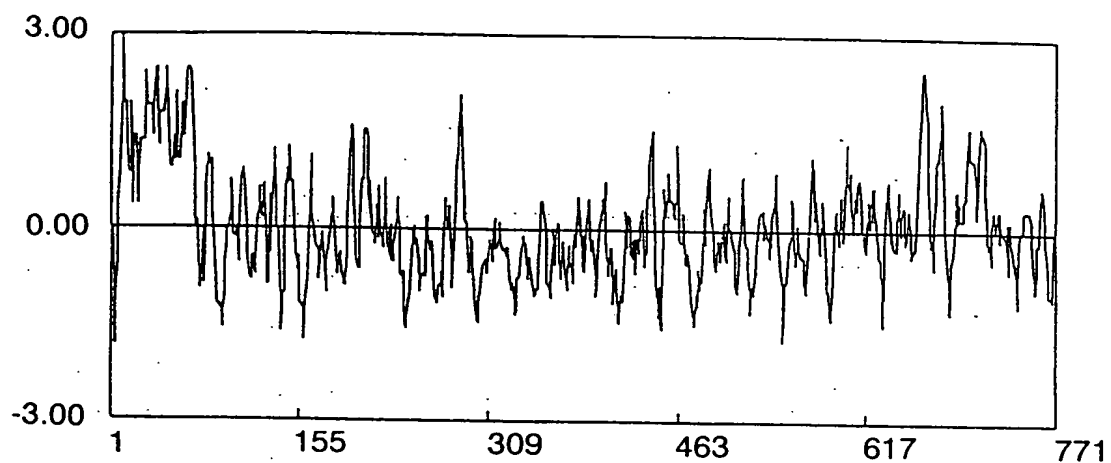


FIG 9

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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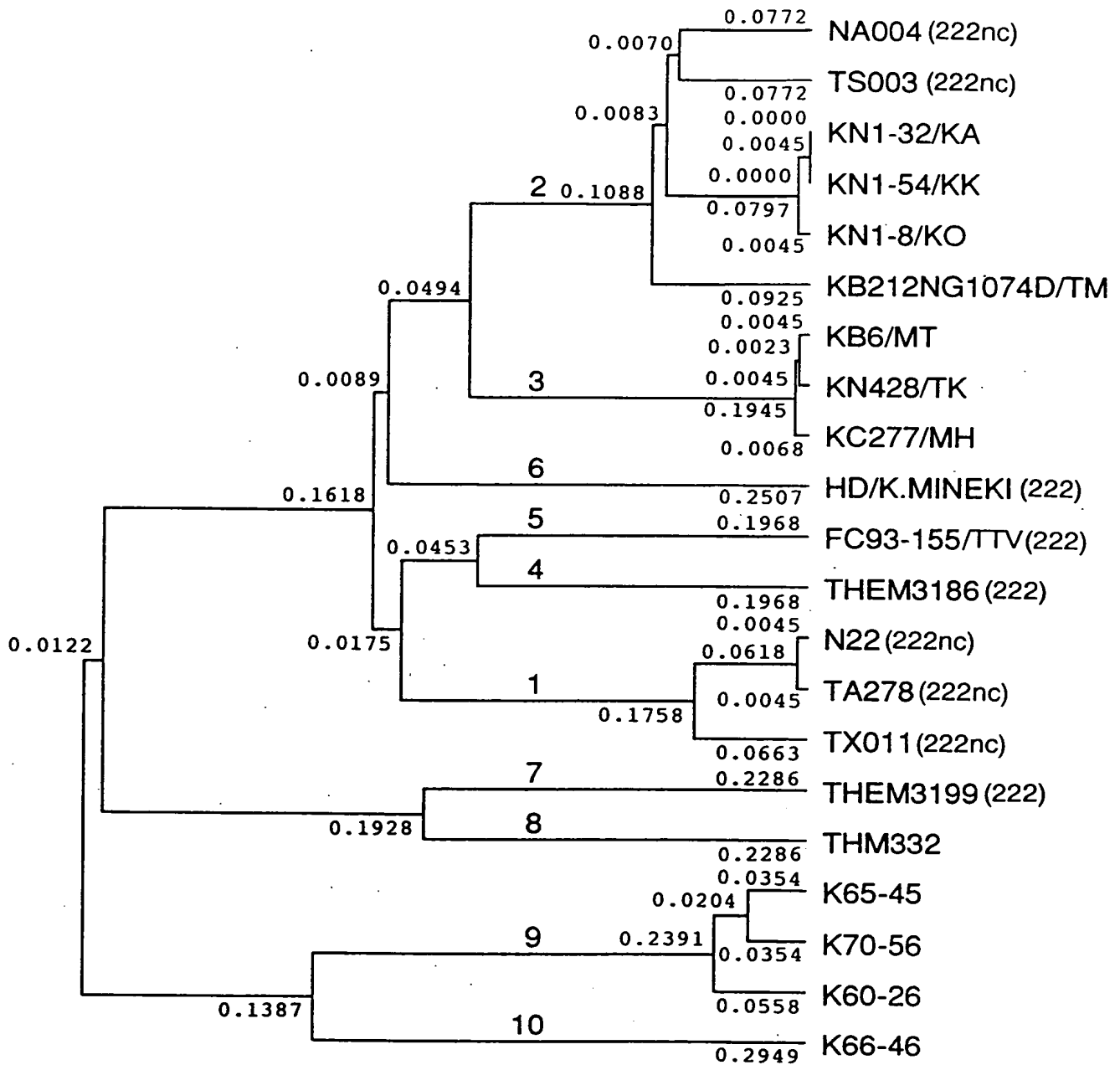


FIG 10

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FIG 11

N2Z(222nc)	1:..CTAAGCAAAAAA..CATGA..CTATGACAA..ACTACAAAGTAAATGCTTAAATATCAGACCTACCTCTATGGCAGCAGCATA	80
TA278(222nc)	1:.....T.....A.....G.G.....G.....C..C..G..G.....A..G.....	80
TX011(222nc)	1:..CT...G.TG..TCAGTA..A.....A.....TC.....GA.A..A.G..CT.G...CT...T...T...	80
TS003(222nc)	1:..CT...G.T..TCAGTA.....AC..G.....TC.C..CA...A.G.C.G..CT.T.TG...	80
NA004(222nc)	1:..C...G.TG..TCAC.G..TCA..GAC..G.C.....TC.C..GAGA..T.G...G...CT...T...	80
KN1-32/KA	1:..C...G.TG..TCAC.G..TCA..GAC..G.C.....TC.C..GAGA..T.G...G...CT...T...	80
KN1-54/KK	1:..C...G.TG..TCAC.G..TCA..GAC..G.C.....TC.C..GA.A..T.G...G..A..CT...T...	80
KN1-8/KO	1:..CT.....T..G..TCAG.A..CTCAC.GAC...C.....TC...G.T..A.G.C...CT...TG...	80
KB212NG1G074D/7M	1:..GTA..G.C.G..TCT.GA.....GAC..GC..C.....C.T...GA.A.A.....TT...T...	80
KB6/MJ	1:..GTA..G.C.G..TCT.GA.....GAC..GC..C.....C.T...GA.A.A.....TT...T...	80
KC277/MH	1:..GTA..G.C.G..TCT.GA.....GAC..GC..C.....C.T...GA.A.A.....C...TT...T...	80
KN428/TK	1:..TCA...TC.G..GCCCTT..CAC...GG.....C.....TGA...TT...T...C..C...CCT.A...	80
THM3186(222)	1:.....TC.G..TGCAGTA..CTCTG..AA.....C.....TGCT.....TT...A.....CT.CTTC.T	80
F93-155/TTV(222)	1:..G.....CC.G...GC.TA..C...CCCTCTA..G..C.....C..C..AA...T.T..C..G...TGATG.T.T	80
HD/K..MNEKI(222)	1:..TGTCCT.....CG.T.CC.CG.TCA..AG.CAC..C.TCC..G.CTACCG..AA...A..C...CTGCTTCAT	80
THM3199(222)	1:..TGC..CT.....TG...CAC.A..TCAGAG.TG..C.CCG.C.G.CT.ACC.....G.C.C..G.AC..G..CCTCT	80
THM332	1:..C..CT..CC.....CAG.G.T...CCTG...GT..C.....TG.....CT...A...A.G...C..CTTC.T	80
K65-45	1:..C..CA...CC.G...CAG.G.T...CCTG...GT..C.....TG..CT..GT...A...A.G...C..CTTC.T	80
X70-56	1:..C..CT...CC.G...CAC.G.T...CCGG...GT..C.....G.....CT...A.T..CT.G...C..CTTT.T	80
K60-26	1:..AC.....GT.....CAG...CTCAGAG.CAG.GGC.TCT..C...C..C..GA...A.G.C..G...CATGA.C..T	80

N22(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
TA278(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
TX011(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
TS003(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
NA004(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN1-32/KK	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN1-54/KK	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN1-8/KO	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KB212NG1074D/TH	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KB6/MT	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KC277/WH	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN428/TK	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
THM3186(222)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
F93-155/TV(222)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
HD/K. MINEXI(222)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
THM3199(222)	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
THM332	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KB65-45	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160
X70-56	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160
KB60-26	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160
KB6-46	81: TGGATATGTAGAAATTTTGTGCAAAAGATACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160

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FIG 12

N22(222nc)	161: CCTTTACAGACCCACAACCTACTAGTACACAGACCCACAAAGGCTTTGTCTTACTCTGTA	222
TA278(222nc)	161:	222
TX011(222nc)	161: T.....C..G..A.....T.....A..C..T...T..	222
TS003(222nc)	161: A.....TA..T..G..G...AC...ACA..AG.CTT.GG..A.AC..A..C...AGCA..	222
NA004(222nc)	161: AC.....TG.....GT...AT...ACA.....CTC.GG..A.AC..G..C...AG..T..T	222
KN1-32/KA	161: AC.....TA.....G..GT...AC...ACA.T...CTC.G...A.AC..A..G...AGCT..T	222
KN1-54/KK	161: AC.....TA.....G..GT...AC...ACA.T...CTC.G...A.AC..A..G...AGCT..T	222
KN1-8/KO	161: AC.....TA.....G..GT...AC...ACA.T...CTC.G...A.AC..A..G...AGCT..T	222
KB212NG1074D/TM	161: A.....TA.....GT...AC...ACA.....CTT.G...T.A.....A..TAG..T..C	222
KB6/MT	161: AC..TACA..T...A.GA...ACAC..AC...TCT..G.....A.AGTA...AGCT..T	222
KC277/MH	161: AC..TACA..T...A.GA...ACAC..AC...TCT..G.....A.AGTA...AGCT..T	222
KN428/TK	161: AC..TACA..T...A.GA...ACAC..AC...TCT..G.....A.AGTA...AGCT..T	222
THEM3186(222)	161: A.AC...T...CATG...G...AC...T..A..GA.CT.C.....A.TG...AGCAA.	222
FC93-155/TTV(222)	161: AC.....G...G..G...AAC...ACA.....T.TC.G..G..C..GTT.....CTAC	222
HD/K.MINEKI(222)	161: G.AC...T...T..G..TA..AA.....ACA.TGA..ACTGG.....C..C..TAGC..A.	222
THEM3199(222)	161: A.AC...A...C...GACCTCGA.AGACA...ACT..TG..A..CA..A..A..TGACTAT	222
THM332	161: A.AC...T..C.CC..CTAT.ACA.AGACA..A.AGAC.TG....ACC.A.....TGACTAC	222
K65-45	161: AC..TC.A..G.CCA.GTACAA..CTGGCA.GGTACA..CT....AC...TTC..TGACACT	225
K70-56	161: AC..TC.G...CCA.GTACAAG..CTGGCAGAATACA...T...AC...TTC..TGACACT	225
K60-26	161: AC..TC.G..G.CCA.GTACAAG..CAGGCA..GTACA..T....A.....TTC..TGACACT	225
K66-46	161: T.AC...T..G..C.CCA.GTAT.ACA.G..TA.....A.AC.GT....AC..AG..A..TGACAC.	225

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NC054 (1) NT01 (795)

1-1/1-9/1-10

NC055 (692)

NC063 (2223)

U17-11/-12/-13

NT04 (2094)

NC021 (3738)

NT03 (2143)

NC065 (3700)

2A-3/2B-1/2B-3

FIG 13

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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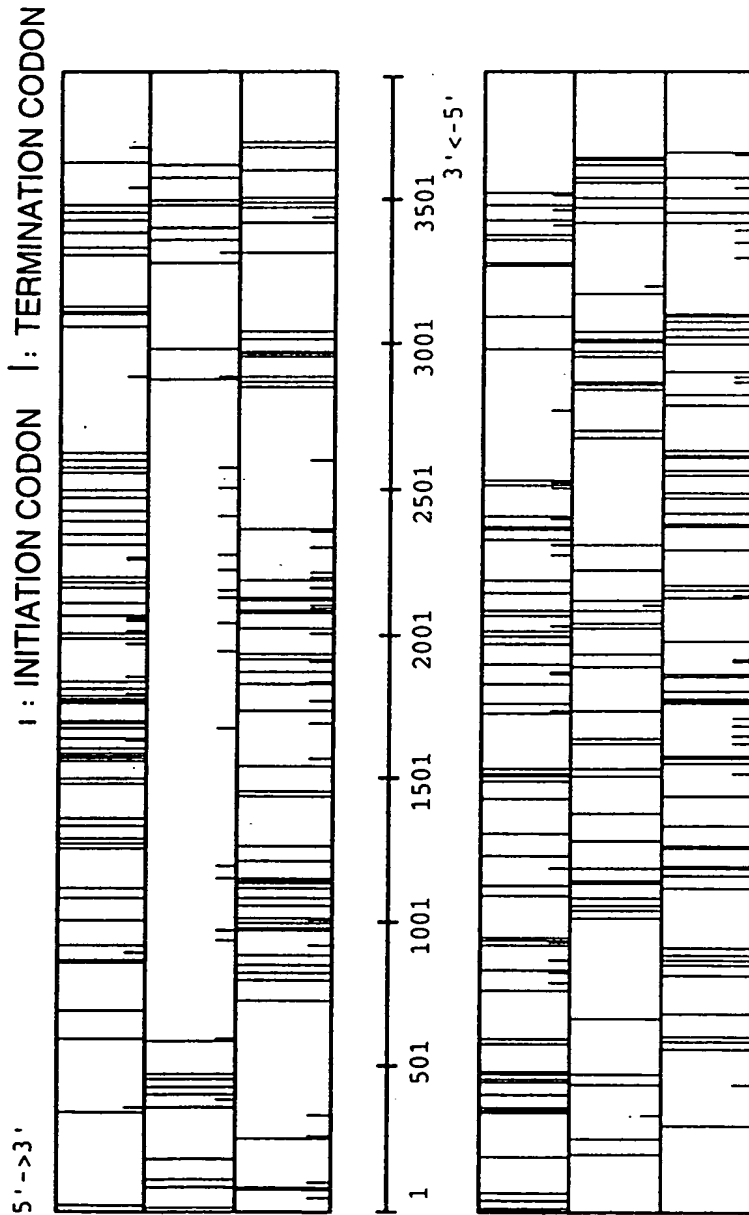


FIG 14

COMPARISON OF 5' END REGION SEQUENCES OF HNT22 (1:) AND TUS01 (2:)

1: ATTTTGCTAC	GTCACCTAAC	ACGTGACACC	CACAGGCCAA	CCGAATGCTA	TGTCA TCCAT	60
2: TTTTGCTAC	GTCACCTAAC	ACGTGACTCC	CGCAGGCCAA	CCGAGTACTA	TGTCGTCCAC	60
1: TTCCTGGGCG	GGGTCTACGT	CCTCATATAA	GTAAGTGAC	TTCCGGAATGG	CTGAGTTTTC	120
2: TTCCTGGGAC	GAGTCTACGT	CCTGATATAA	GTAAGTGAC	TTCCGGAATGG	CTGAGTTTTC	120
1: CACGCCCGTC	CGCAGCGGTG	AA GCCACGG	AGGGAGATC	TC CGCGTCC	CGAGGCGGG	180
2: CACGCCCGTC	CGCAGCGGAG	AA GCGCACGG	AGGGAGATC	TC CGCGTCC	CGAGGCGGG	180
1: TGCCGAAGGT	GAGTTTACAC	ACCGAAGTCA	AGGGCAATT	CGGGCTCGGG	ACTGGCCGGG	240
2: TGCCGAAGGT	GAGTTTACAC	ACCGAAGTCA	AGGGCAATT	CGGGCTCGGG	ACTGGCCGGG	240
1: CTATGGGCAA	GGCTCTGAAA	AAA GCA TGT	TTAT TGGCAG	GCA TTA CAGA	AAGAAAAGGG	300
2: CCGCGGGCAA	GGCTCTTAAA	AAATGCAC-T	TTCT-G-CAG	--AGTGC-GA	GCGAAAAGGA	300

FIG 15

COMPARISON OF 3' END REGION SEQUENCES OF HNT22 (1:) AND TUS01 (2:)

1: TAA--TATGA	CA TGT TTT TGGT	GACCCCAAT	CTACACCC	TTCAGTAA	GACTGGGAA	60
1: AGGAGTACCA	GTGCTGTAGA	ATATGGGACA	GACCCCTAG	AGGCAACCTA	AGAGATACCC	120
1: CTTTCTACCC	CTGGGTACCT	CAAGCAAAAC	CTAGTACCG	TGTAACTTT	AAACTTGGAT	180
1: TCAATAAAG	CTAGGCGGTG	GGAGTTTCA	TTGTGGGTG	CTGCTTATA	AGTAACTAA	240
1: GCACTCCGAG	CGTAAGCGAG	GGTGGGACC	CTGGGCTG	GGGCAACTCC	TTCGGAGTCC	300
1: GCGGCTACGC	GCCTTCCGCT	GGCGCGGCA	CTCAGACCC	CCGCTCGTGC	TGAACCGCT	360
1: GCGGCTTTCG	GACCACTTCC	GGTCCGGGG	GGTCCGGGAA	TTTACTAAAC	AGACTCCGAG	420
1: TTGCCATTGG	ACTCATGAGG	TATGAATCAG	TAAACGAAAGT	GAGTGGGGCC	AGACTTCCGC	480
1: ATAAGGCTTT	TATCTTCTTG	CCATTTGTCA	GTAAAGAGGG	TCCGCTATAG	CTTCCGCCCTC	540
1: CACTTTTACCT	TCTATAAAACT	ACCAAAATGG	CCGTTCAGT	GACGTACACAG	CCGCCATTITT	600
1: AAGTAGCTGA	CGTCAAGGAT	TGACGTAAAG	GTAAAGGTC	ATCCTCGGCG	GAACTACAC	660
1: AAAATGGTGG	ACAAATCTT	CCGGTCAAA	GGTGTGCTC	ACGTCAATAAG	TCACTGGAG	720
1: GGGACCCGCT	GTAAACCGGA	AGTAGGCCCC	GTACCGTGA	TTGCTCACGTC	TGTACACGTC	780
1: ACAACCGCCA	TTTGTGTTTA	CAAAATGGCT	GACTTCCCTTC	CTCTTTT	AAAAAAGGCG	840
1: CCAAAACAC	GTCCGGC	855				

FIG 16